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Draft Genome Sequence of *Propionibacterium acnes* subsp. *elongatum* Strain Asn12

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ABSTRACT *Propionibacterium acnes*, a non-spore-forming anaerobic Gram-positive bacterium, has been linked to a wide range of opportunistic human infections and conditions, most notably acne vulgaris. Here, we present the draft genome sequence of *P. acnes* subsp. *elongatum* strain Asn12, isolated from spinal disc tissue (in the United Kingdom).

The Gram-positive anaerobic bacterium *Propionibacterium acnes* forms part of the normal microbiota on human skin and mucosal surfaces. While normally associated with skin health, *P. acnes* is also an opportunistic pathogen linked with a range of human infections and clinical conditions, such as acne vulgaris (1), prosthetic joint infection (2), prostate cancer (3), sarcoidosis (4), progressive macular hypomelanosis (PMH) (5), and degenerative disc disease (6). Ever since we showed that distinct strains of *P. acnes* induce different gene expression patterns in human keratinocytes (7) and sebocytes (8), further advances in our understanding of the intraspecies phylogeny of *P. acnes* have occurred. Distinct phylogroups have been discovered and specific strains or sequence types (STs) associated with human health or disease revealed (9). In-depth studies of the phylogenetic and taxonomic heterogeneity of *P. acnes* have ultimately led to the recent proposal of the type I, II, and III phylogroups as distinct subspecies known as *P. acnes* subsp. *acnes*, *P. acnes* subsp. *defendens*, and *P. acnes* subsp. *elongatum*, respectively.

Here, we present the draft genome sequence of *P. acnes* subsp. *elongatum* strain Asn12 (10) that was isolated from spinal disc tissue (in the United Kingdom). The culture conditions and genomic DNA isolation methods were as published previously (11, 12). Sequencing libraries with ~500-bp inserts were prepared from 500 ng of input DNA using the NEBNext DNA library prep master mix for Illumina. Genome sequencing was performed on an Illumina MiSeq instrument, which generated 1,380,920 2 × 250-bp reads and yielded ~95-fold coverage. Assembly was performed using the Genomics Workbench 11.0 (Qiagen). Gap closing was accomplished using PCR (primers are available on request), followed by Sanger sequencing, as described previously (13). Automatic annotation of the genome was performed using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) version 4.5 (<https://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). We have assembled the genome of *P. acnes* subsp. *elongatum* strain Asn12 into 2 contigs, with 2,484,878 bp, 2,422 putative coding sequences, 45 tRNAs, and 9 rRNAs.

To date, the majority of the *P. acnes* genomes sequenced belong to *P. acnes* subsp. *acnes*, with only four genomes of *P. acnes* subsp. *elongatum* strains (HL201PA1,

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JCM18909, PMH5, and PMH7) available (14, 15). This is not surprising since this subspecies has rarely been cultured from healthy facial skin, which is a primary skin sampling site, or from opportunistic infections or acne patients; strains from this subspecies, however, have been recently linked with the skin condition PMH (5, 16). Furthermore, type III strains are more frequently found on the back and abdomen than on other body sites, suggesting that this may be their preferred niche (16). *P. acnes* subsp. *elongatum* strain Asn12 belongs to ribotype 9 and, on the basis of our eight-gene multilocus sequence typing (MLST₈) scheme (17), belongs to the ST33 lineage and clonal complex 77. As isolates PMH5 and PMH7 also belong to ST33, it will be of particular importance to sequence *P. acnes* subsp. *elongatum* isolates from other STs.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [QKRC00000000](https://www.ncbi.nlm.nih.gov/nuccore/QKRC00000000). The version described in this paper is version QKRC01000000.

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